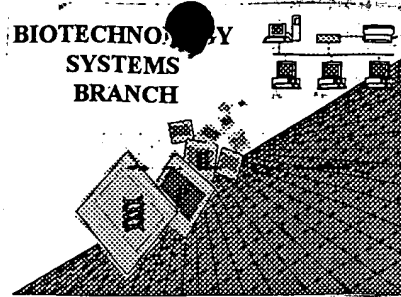


Q. Nguyen

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/578,656
Source: 1632
Date Processed by STIC: 11/30/2000

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TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

P. Nguyen

#4
12-14-00
1632 P. Z

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/578,656
DATE: 11/30/2000
TIME: 11:00:20

Input Set : A:\4910-3-SequenceListing.txt
Output Set: N:\CRF3\11302000\I578656.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Li, Hung
5 Hsieh-Li, Hsiu-Mei
6 Chang, Jan-Gowth
7 Jong, Yuh-Jyh
8 Wu, Mei-Hsiang
9 Tsai, Chang-Hai
11 <120> TITLE OF INVENTION: A Knockout-Transgenic Mouse Model of Spinal Muscular Atrophy
W--> 12 <130> FILE REFERENCE: 4910-3
W--> 13 <140> CURRENT APPLICATION NUMBER: US 09/578,656
14 <141> CURRENT FILING DATE: 2000-05-25
15 <150> PRIOR APPLICATION NUMBER: US 60/136,520
16 <151> PRIOR FILING DATE: 1999-05-28
W--> 17 <160> NUMBER OF SEQ ID: 15

ERRORED SEQUENCES

19 <210> SEQ ID NO: 1
20 <211> LENGTH: 21
21 <212> TYPE: DNA
22 <213> ORGANISM: Artificial Sequence
W--> 23 <220> FEATURE:
24 <223> OTHER INFORMATION: Primer for PCR
W--> 25 <400> SEQUENCE: 1
E--> 26 ataacaccac cactcttact c
29 <210> SEQ ID NO: 2
30 <211> LENGTH: 21
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial Sequence
W--> 33 <220> FEATURE:
34 <223> OTHER INFORMATION: Primer for PCR
W--> 35 <400> SEQUENCE: 2
E--> 36 gtagecgtga tgccattgtc a
39 <210> SEQ ID NO: 3
40 <211> LENGTH: 21
41 <212> TYPE: DNA
42 <213> ORGANISM: Artificial Sequence
W--> 43 <220> FEATURE:
44 <223> OTHER INFORMATION: Primer for PCR
W--> 45 <400> SEQUENCE: 3
E--> 46 agcctgaaga acgagatcag c
48 <210> SEQ ID NO: 4
49 <211> LENGTH: 24
50 <212> TYPE: DNA
51 <213> ORGANISM: Artificial Sequence
W--> 52 <220> FEATURE:
53 <223> OTHER INFORMATION: Primer for PCR

Per 1.822 of Sequence Rules,
insert cumulative base total
at right margin of
each line

21

21

21

global error

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/578,656

DATE: 11/30/2000
TIME: 11:00:20

Input Set : A:\4910-3-SequenceListing.txt
Output Set : N:\CRF3\11302000\I578656.raw

```

W--> 54 <400> SEQUENCE: 4
E--> 55 actgcaacct cctgggttca agtg
      58 <210> SEQ ID NO: 5
      59 <211> LENGTH: 24
      60 <212> TYPE: DNA
      61 <213> ORGANISM: Artificial Sequence
W--> 62 <220> FEATURE:
      63 <223> OTHER INFORMATION: Primer for PCR
W--> 64 <400> SEQUENCE: 5
E--> 65 cagttcgaga ccagcctgac caat
      68 <210> SEQ ID NO: 6
      69 <211> LENGTH: 25
      70 <212> TYPE: DNA
      71 <213> ORGANISM: Artificial Sequence
W--> 72 <220> FEATURE:
      73 <223> OTHER INFORMATION: Primer for PCR
W--> 74 <400> SEQUENCE: 6
E--> 75 cgaatcactt gagggcagga gtttg
      78 <210> SEQ ID NO: 7
      79 <211> LENGTH: 25
      80 <212> TYPE: DNA
      81 <213> ORGANISM: Artificial Sequence
W--> 82 <220> FEATURE:
      83 <223> OTHER INFORMATION: Primer for PCR
W--> 84 <400> SEQUENCE: 7
E--> 85 aactggtgga catggctggt cattg
      88 <210> SEQ ID NO: 8
      89 <211> LENGTH: 25
      90 <212> TYPE: DNA
      91 <213> ORGANISM: Artificial Sequence
W--> 92 <220> FEATURE:
      93 <223> OTHER INFORMATION: Primer for PCR
W--> 94 <400> SEQUENCE: 8
E--> 95 aaaccagtcg ggcacaatac ctacg
      98 <210> SEQ ID NO: 9
      99 <211> LENGTH: 24
      100 <212> TYPE: DNA
      101 <213> ORGANISM: Artificial Sequence
W--> 102 <220> FEATURE:
      103 <223> OTHER INFORMATION: Primer for PCR
W--> 104 <400> SEQUENCE: 9
E--> 105 tatgctgatt gaaggagggt gtgc
      108 <210> SEQ ID NO: 10
      109 <211> LENGTH: 28
      110 <212> TYPE: DNA
      111 <213> ORGANISM: Artificial Sequence
W--> 112 <220> FEATURE:
      113 <223> OTHER INFORMATION: Primer for PCR
W--> 114 <400> SEQUENCE: 10

```

24 ← insert

24

insert
cumulative
base totals
globally

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/578,656

DATE: 11/30/2000
TIME: 11:00:20

Input Set : A:\4910-3-SequenceListing.txt
Output Set : N:\CRF3\11302000\i578656.raw

E--> 115 cgctgcgcac ccgcgggttt gctatggc
118 <210> SEQ ID NO: 11
119 <211> LENGTH: 21
120 <212> TYPE: DNA
121 <213> ORGANISM: Artificial Sequence
W--> 122 <220> FEATURE:
123 <223> OTHER INFORMATION: Primer for PCR
W--> 124 <400> SEQUENCE: 11
E--> 125 tcccagtcctt gccctggca t
128 <210> SEQ ID NO: 12
129 <211> LENGTH: 20
130 <212> TYPE: DNA
131 <213> ORGANISM: Artificial Sequence
W--> 132 <220> FEATURE:
133 <223> OTHER INFORMATION: Primer for PCR
W--> 134 <400> SEQUENCE: 12
E--> 135 aacatcaagc ccaaatctgc
138 <210> SEQ ID NO: 13
139 <211> LENGTH: 29
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
W--> 142 <220> FEATURE:
143 <223> OTHER INFORMATION: Primer for PCR
W--> 144 <400> SEQUENCE: 13
E--> 145 gccagtatga tagccactca tgtaccatg
148 <210> SEQ ID NO: 14
149 <211> LENGTH: 31
150 <212> TYPE: DNA
151 <213> ORGANISM: Artificial Sequence
W--> 152 <220> FEATURE:
153 <223> OTHER INFORMATION: Primer for PCR
W--> 154 <400> SEQUENCE: 14
E--> 155 ctcccatatg tccagattct cttgatgatg c
158 <210> SEQ ID NO: 15
159 <211> LENGTH: 21
160 <212> TYPE: DNA
161 <213> ORGANISM: Artificial Sequence
W--> 162 <220> FEATURE:
163 <223> OTHER INFORMATION: Primer for PCR
W--> 164 <400> SEQUENCE: 15
E--> 165 actgcctcac caccgtgctg g

*insert
base totals
globally*

VERIFICATION SUMMARY

DATE: 11/30/2000

PATENT APPLICATION: US/09/578,656

TIME: 11:00:21

Input Set : A:\4910-3-SequenceListing.txt

Output Set: N:\CRF3\11302000\I578656.raw

L:12 M:283 W: Missing Blank Line separator, <130> field identifier
L:13 M:283 W: Missing Blank Line separator, <140> field identifier
L:17 M:283 W: Missing Blank Line separator, <160> field identifier
L:23 M:283 W: Missing Blank Line separator, <220> field identifier
L:25 M:283 W: Missing Blank Line separator, <400> field identifier
L:26 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:1
L:33 M:283 W: Missing Blank Line separator, <220> field identifier
L:35 M:283 W: Missing Blank Line separator, <400> field identifier
L:36 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:2
L:43 M:283 W: Missing Blank Line separator, <220> field identifier
L:45 M:283 W: Missing Blank Line separator, <400> field identifier
L:46 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:3
L:52 M:283 W: Missing Blank Line separator, <220> field identifier
L:54 M:283 W: Missing Blank Line separator, <400> field identifier
L:55 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:4
L:62 M:283 W: Missing Blank Line separator, <220> field identifier
L:64 M:283 W: Missing Blank Line separator, <400> field identifier
L:65 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:5
L:72 M:283 W: Missing Blank Line separator, <220> field identifier
L:74 M:283 W: Missing Blank Line separator, <400> field identifier
L:75 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:6
L:82 M:283 W: Missing Blank Line separator, <220> field identifier
L:84 M:283 W: Missing Blank Line separator, <400> field identifier
L:85 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:7
L:92 M:283 W: Missing Blank Line separator, <220> field identifier
L:94 M:283 W: Missing Blank Line separator, <400> field identifier
L:95 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:8
L:102 M:283 W: Missing Blank Line separator, <220> field identifier
L:104 M:283 W: Missing Blank Line separator, <400> field identifier
L:105 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:9
L:112 M:283 W: Missing Blank Line separator, <220> field identifier
L:114 M:283 W: Missing Blank Line separator, <400> field identifier
L:115 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:10
L:122 M:283 W: Missing Blank Line separator, <220> field identifier
L:124 M:283 W: Missing Blank Line separator, <400> field identifier
L:125 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:11
L:132 M:283 W: Missing Blank Line separator, <220> field identifier
L:134 M:283 W: Missing Blank Line separator, <400> field identifier
L:135 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:12
L:142 M:283 W: Missing Blank Line separator, <220> field identifier
L:144 M:283 W: Missing Blank Line separator, <400> field identifier
L:145 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:13
L:152 M:283 W: Missing Blank Line separator, <220> field identifier
L:154 M:283 W: Missing Blank Line separator, <400> field identifier
L:155 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:31 SEQ:14
L:162 M:283 W: Missing Blank Line separator, <220> field identifier
L:164 M:283 W: Missing Blank Line separator, <400> field identifier
L:165 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:15

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